

## A New Species of the *Gekko japonicus* Group (Squamata: Gekkonidae) from Southwest China

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**Abstract** A new species of the *Gekko* (Squamata: Gekkonidae) is described from the border of Sichuan and Yunnan Province, southwest China, based on distinct morphological and molecular features. *Gekko jinjiangensis* sp. nov. is distinguished from congeners by a combination of the following characters: size small (SVL 50.2–61.6 mm,  $n = 13$ ); nares in contact with rostral; interorbital scales between anterior corners of the eyes 20–24; ventral scales between mental and cloacal slit 146–169; midbody scale rows 111–149; ventral scale rows 31–47; subdigital lamellae on first toe 8–11, on fourth toe 11–15; no webbing in the fingers and toes; with tubercles on upper surface of fore and hind limbs; precloacal pores 4–5 in males; postcloacal unilateral tubercles 1–2; dorsal surface of body with 8–9 large greyish brown markings between nape and sacrum. In molecular analyses, the new species is sister to *G. scabridus*, but separated from them by approximately 9.9%–12.2% in genetic divergence as shown by a fragment of the partial mitochondrial ND2 gene. The new species is the highest *Gekko* with elevation range from 2000 to 2476 m. Further surveys are recommended to better understand the occurrence and population status of the new species.

**Keywords** *Gekko jinjiangensis* sp. nov., *Gekko japonicus* group, molecular phylogenetic analysis, morphology, Jinsha River

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Received: 30 May 2020 Accepted: 9 September 2020

### 1. Introduction

The genus *Gekko* Laurenti, 1768 belongs to Gekkonidae Gray, 1825 of Sauria (Lacertilia), distributed across tropical Asia and western Oceania, from India eastwards to Melanesia. The genus currently contains 77 species, of which 19 species are known from China (Uetz, 2020). Wood *et al.* (2020) presented a new classification emphasizing the most inclusive, original generic name (*Gekko*) for these ~60 taxa, arranged into seven subgenera: Subgenus *Gekko*, *Japonigekko*, *Ptychozoon*, *Rhacogekko*, *Lomatodactylus*, *Balawangekko*, *Archipelagekko*. From the phylogenetic relationship, the subgenus *Japonigekko* is equivalent in content to the *Gekko japonicus* Group (Wood *et al.*, 2020). *G. japonicus* group is the most diverse group in the genus *Gekko*, which have a wide distribution in eastern Asia, from China eastwards to Japan, southwards to Vietnam and Laos (Rösler *et al.*, 2011; Luu *et al.*, 2015). The members of this group are characterized by a moderate size; nares usually in contact with rostral; two or three nasals; 0–21 rows of dorsal tubercles; 0–32 precloacal pores; 1–4 postcloacal tubercles; the webbing between fingers and toes weakly to extensively developed; lateral folds without tuber. The *Gekko japonicus* group currently contains 27 described species (Luu *et al.*, 2017; Wood *et al.*, 2020).

The Jinsha River basin locates in the Mountains of Southwest China, which is one of biodiversity hotspots and one of the most concentrated and vulnerable areas of the forest ecosystem along the Yangtze River. During the field surveys in 2019 in the Jinsha River region, near the border of Sichuan

and Yunnan Province (Prov.), China, a series of gekkonid specimens were collected in the middle reaches of the Jinsha River. Morphologically, these specimens can be assigned to the *Gekko japonicus* group based on the following features: size small; nare in contact with rostral; postcloacal tubercles present; no webbing between fingers and toes; lateral folds without tubercles; subcaudals enlarged; dorsum with bands (Rösler *et al.*, 2011; Nguyen *et al.*, 2013).

Molecular data showed that the specimens from Sichuan and Yunnan Province were clustered in the same clade with *Gekko scabridus*, the specimens are monophyletic and compose the sister species to *G. scabridus*. And, the molecular divergence calculated using data from a fragment of the mitochondrial NADH dehydrogenase subunit 2 (ND2) gene between the two species is approximately 9.9%–12.2%, it is much higher than the threshold interspecific separation of *G. japonicus* group in *Gekko* species from ND2, which is approximately 6.6% (Luu *et al.*, 2015, 2017). From the morphological comparisons and molecular phylogenetic analyses, we indicate that the specimens should represent an undescribed species.

## 2. Materials and Methods

**2.1. Sample preparation** Thirteen adult individuals (9 females, 4 males) of the undescribed species were collected in August

and September, 2019 in the Jinsha River region, between the border of Sichuan and Yunnan Prov., China (Table 1). For comparisons, some specimens of congeneric species were also collected, *G. scabridus* from Panzhihua (Yanbian), Sichuan Prov. (The collection site is located between the two type locations Yongren and Miyi). After taking photographs, the individuals were euthanized using isoflurane, and the specimens were then fixed with 10% formalin and preserved in 75% ethanol. Liver tissue samples were taken and preserved separately in 95% ethanol prior to fixation. Specimens were deposited in Chengdu Institute of Biology, Chinese Academy of Sciences (CIB, CAS).

**2.2. Molecular data and phylogenetic analyses** Genomic DNA from each specimen was extracted using a TIANamp Genomic DNA Kit by TIANGEN (BEIJING) BIOTECH, China. The fragment of NADH dehydrogenase subunit 2 (ND2) gene was amplified using the primer pairs L4437b (Macey *et al.*, 1997) and ND2r102 (Greenbaum *et al.*, 2007). PCR amplifications were performed in a reaction volume of 25  $\mu$ l. Fragments were amplified under the following conditions: for ND2, an initial denaturing step at 95 °C for 2 min; 32 cycles of denaturing at 95 °C for 35 s, annealing at 50 °C for 35 s and extending at 72 °C for 95 s. Sequencing was conducted using an ABI3730 automated DNA sequencer in Shanghai DNA BioTechnologies Co., Ltd. (Shanghai, China). New sequences were deposited in GenBank (for GenBank accession numbers see Table 1).

**Table 1** Samples used in the molecular analyses, including their GenBank accession No., Voucher No. and locality. “/” means no available data.

Species	Voucher No.	Locality	GenBank accession No. (ND2)	Sources
<i>Gekko scabridus</i>	CIBYN201909199	Yanbian, Panzhihua, Sichuan, China	MT449429	This study
<i>Gekko scabridus</i>	CIBYN201909200	Yanbian, Panzhihua, Sichuan, China	MT449430	This study
<i>Gekko jinjiangensis</i> sp. nov.	CIB5334220115	Deqin, Diqing, Yunnan, China	MT449431	This study
<i>Gekko jinjiangensis</i> sp. nov.	CIB5334220088	Deqin, Diqing, Yunnan, China	MT449432	This study
<i>Gekko jinjiangensis</i> sp. nov.	CIB5334220089	Deqin, Diqing, Yunnan, China	MT449433	This study
<i>Gekko jinjiangensis</i> sp. nov.	CIB5334220090	Deqin, Diqing, Yunnan, China	MT449434	This study
<i>Gekko jinjiangensis</i> sp. nov.	CIB5334220100	Deqin, Diqing, Yunnan, China	MT449435	This study
<i>Gekko jinjiangensis</i> sp. nov.	CIB5334220114	Deqin, Diqing, Yunnan, China	MT449436	This study
<i>Gekko jinjiangensis</i> sp. nov.	CIB5133380017	Derong, Sichuan, China	MT449437	This study
<i>Gekko jinjiangensis</i> sp. nov.	CIB5133380019	Derong, Sichuan, China	MT449438	This study
<i>Gekko jinjiangensis</i> sp. nov.	CIB5133380021	Derong, Sichuan, China	MT449439	This study
<i>Gekko jinjiangensis</i> sp. nov.	CIB5133380024	Derong, Sichuan, China	MT449440	This study
<i>Gekko jinjiangensis</i> sp. nov.	CIB5133380025	Derong, Sichuan, China	MT449441	This study
<i>Gekko jinjiangensis</i> sp. nov.	CIB5133380026	Derong, Sichuan, China	MT449442	This study
<i>Gekko jinjiangensis</i> sp. nov.	CIB5133380047	Derong, Sichuan, China	MT449443	This study
<i>Gekko japonicus</i>	NNU Z20050801.004	Zhoushan, Zhejiang, China	JN019059	Rösler <i>et al.</i> , 2011
<i>Gekko hokouensis</i>	NNU Z20050902.001	Jinzhai, Anhui, China	JN019060	Rösler <i>et al.</i> , 2011
<i>Gekko swinhonis</i>	NNU Z20051124.001	Bo'ai, Henan, China	JN019061	Rösler <i>et al.</i> , 2011
<i>Gekko auriverrucosus</i>	NNU Z20050716.004	Yuncheng, Shanxi, China	JN019062	Rösler <i>et al.</i> , 2011
<i>Gekko subpalmatus</i>	AMB 6567	Chengdu, Sichuan, China	JN019063	Rösler <i>et al.</i> , 2011
<i>Gekko japonicus</i>	HOFH 10061401	Ryukyu Islands	JQ173423	Siler <i>et al.</i> , 2012
<i>Gekko japonicus</i>	/	Fukuoka, Japan	MN811642	Kim <i>et al.</i> , 2020
<i>Gekko chinensis</i>	LSUHC 4210	Wuzhi Shan, Hainan Island, China	JQ173409	Siler <i>et al.</i> , 2012
<i>Lepidodactylus moestus</i>	USNM 521730	Ngerur Island, Palau	JN019079	Rösler <i>et al.</i> , 2011

For molecular analyses, the available sequence data for all related species of the genus were downloaded from GenBank. For phylogenetic analyses, the available sequence data of *Lepidodactylus moestus* (Peters, 1867) was downloaded, and used as outgroup (All GenBank accession number see Table 1).

Sequences were assembled and aligned using the Clustalw options in BioEdit v. 7.0.9.0 (Hall, 1999) with default settings. Alignments were checked by eye and modified manually if necessary. Phylogenetic analyses were conducted using maximum likelihood (ML) and Bayesian Inference (BI) methods, implemented in PHYML Online execution (Guindon *et al.*, 2010) and MrBayes 3.2.2 (Ronquist *et al.*, 2012), respectively. The maximum likelihood (ML) analyses in PhyML software, with NNI search, automatic model selection by SMS (Smart Model Selection), under a GTR+ G + I substitution model. The reliability of the phylogenies was estimated with the approximate likelihood-ratio (aLRT) SH-like test (Anisimova and Gascuel, 2006). In BI analyses, two runs each with four Markov chains were run for 20 million iterations with sampling every 1000 generations. The first 25% of generations were removed as the “burn-in” stage followed by calculation of Bayesian posterior probabilities and the 50% majority-rule consensus of the post burn-in trees sampled at stationarity. Trees were visualized with FigTree v1.4.2 program (Rambaut, 2012). Genetic distance was calculated with the pairwise

uncorrected *p*-distance model between *Gekko* species on ND2 gene using MEGA v. 7 (Kumar *et al.*, 2016).

**2.3. Morphological comparisons** A total of 13 adult specimens (9 females and 4 males) representing the type series of undescribed species (for voucher information see Table 1). The terminology and methods followed Rösler *et al.* (Rösler *et al.*, 2011). Sex was determined by presence of precloacal pores. Morphological data of the *G. scabridus* were obtained from specimens near type locality (see Table 1) and literatures (Zhou *et al.*, 1982; Zhao *et al.*, 1999). For other species, data cited from literatures (Stejneger, 1901; Zhou *et al.*, 1982; Song, 1985; Zhao *et al.*, 1999; Goris and Maeda, 2004; Rösler *et al.*, 2004; Toda *et al.*, 2008; Zhou and Wang, 2008; Rösler *et al.*, 2010; Phung and Ziegler, 2011; Nguyen *et al.*, 2013; Luu *et al.*, 2014; Ngo *et al.*, 2015; Yang, 2015; Luu *et al.*, 2015, 2017).

**2.4. Morphological characters** Measurements were taken with digital calipers to the nearest 0.1 mm. In total, 32 morphometric characters of adult specimen were measured. The following abbreviations were used (Table 2):

### 3. Results

**3.1. Phylogenetic analyses** Aligned sequences matrix of ND2 contained 552 bp. ML and BI trees presented similar topology (Figure 1). The *G. japonicus* group was strongly supported as

**Table 2** Morphological characters and abbreviations used in this study. Bilateral scale counts were given as left/right.

Abbreviations	Characters	Scalation	Characters
SVL	snout vent length (from tip of snout to anterior margin of cloaca)	CS	ciliary spines
TaL	tail length (from posterior margin of cloaca to tip of tail)	N	nasals (nasorostrals, supranasals, postnasals)
AG	distance between axilla and groin	I	intersupranasals (scales between supranasals, in contact with rostral)
HL	maximum head length (from tip of snout to posterior margin of auricular opening)	SPL	supralabials
HW	maximum head width	IFL	infralabials
HH	maximum head height	IO	interorbitals (number of scales in a line between anterior corners of eyes)
SE	distance from snout tip to anterior corner of eye	PO	preorbitals (number of scales in a line from nostril to anterior corner of the eye)
EE	distance between posterior margin of eye to posterior margin of ear opening	PM	postmentals
RW	maximum rostral width	GP	gulars bordering the postmentals
RH	maximum rostral height	DTR	dorsal tubercle rows at midbody
MW	maximum mental width	GSDT	granules surrounding dorsal tubercles
ML	maximum mental length	SMC	scales in a line from mental to the front of cloacal slit
		SR	scale rows at midbody (including ventral scales)
		V	ventral scale rows at midbody
		LF1	subdigital lamellae under first finger
		LF4	subdigital lamellae under fourth finger
		LT1	subdigital lamellae under first toe
		LT4	subdigital lamellae under fourth toe
		PP	precloacal pores
		PAT	postcloacal tubercles

a monophyletic group. All 13 specimens of the new species forms an independent clade, and nested in the *G. japonicus* group, sister to *G. scabridus*. Uncorrected pairwise divergences within these specimens range from 0% to 3.6% (Table 3). The uncorrected *p*-distance between the undescribed species and other known species from the *G. japonicus* group range from 9.9% (*G. scabridus*) to 27.0% (*G. auriverrucosus* and *G. chinensis*), which is among inter-species level (Luu *et al.*, 2015, 2017). Herein, we describe these specimens as a new species.

### 3.2. Morphological analyses

#### Taxonomic accounts

##### *Gekko jinjiangensis* sp. nov. HOU, SHI, WANG, JIANG and XIE

*Gekko japonicus* Yang and Rao, 2008. Amphibian and reptilia of Yunnan. 177–181.

**Holotype** CIB5334220115 (Figure 2), adult male, from BaiSheng Village, Benzilan Town, (28.23463° N, 99.30227° E, 2045 m a. s. l.), Deqin County, Yunnan Prov., China, collected by Shengchao SHI, Jianyi FENG, Lei FU on 25 August 2019.

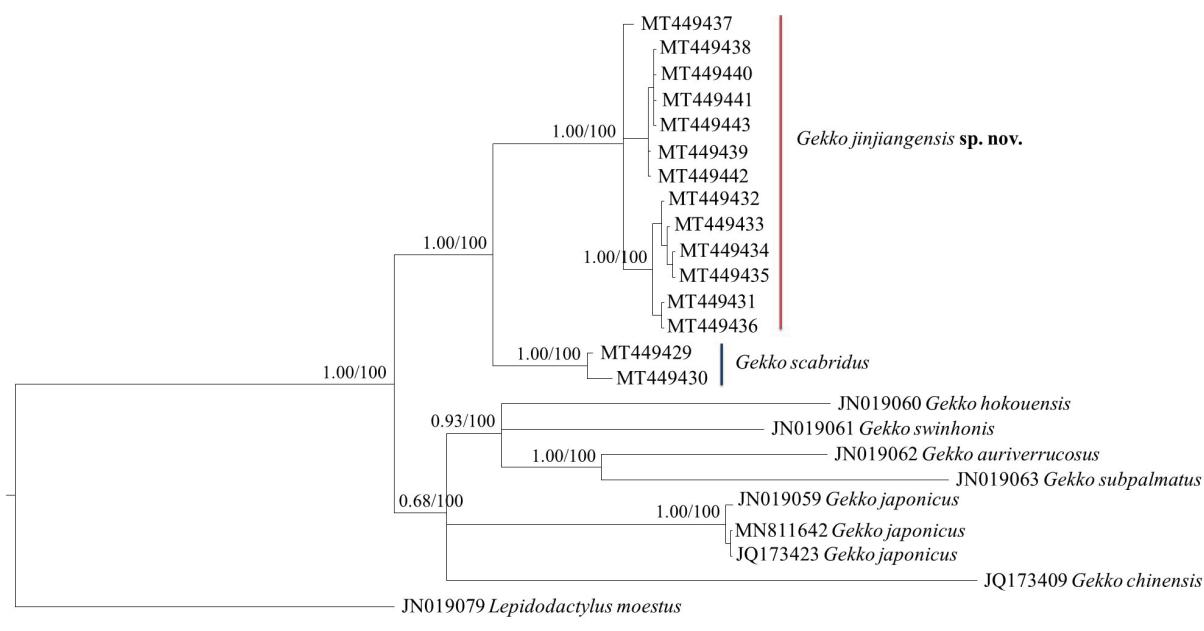
**Paratype** Twelve adults (9 females and 3 males), collected from the two places. Specimen CIB5334220088-90, CIB5334220100, CIB5334220114 were collected from Benzilan Town (Diqing Tibetan Autonomous Prefecture), Yunnan Prov. by Shengchao SHI, Jianyi FENG, Lei FU on 27 August, 2019. CIB5133380017, CIB5133380019, CIB5133380021, CIB5133380024–26, CIB5133380047 were collected from Guxue Town (Derong County 28.424694° N, 99.263363° E, 2114 m a. s. l.), Sichuan Prov.

by Gang WANG, Yinmeng HOU, Fuxuan LIANG, Yusong TANG on 26 August, 2019.

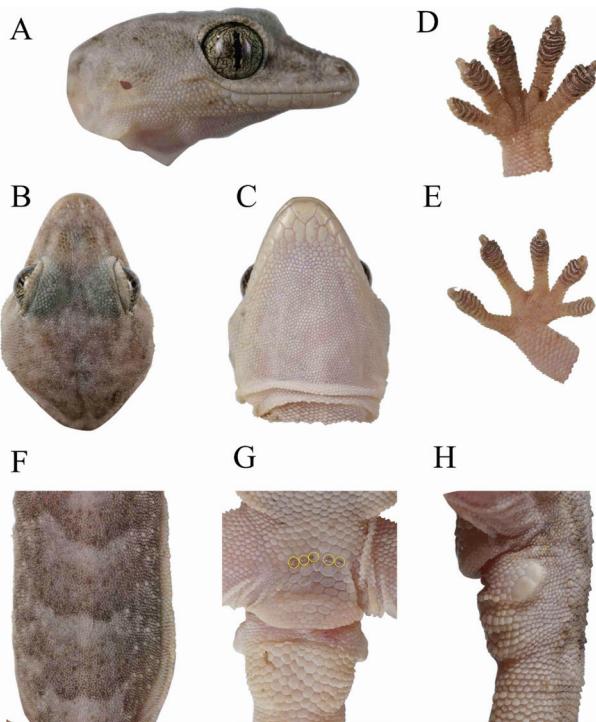
**Etymology** The specific epithet *jinjiangensis* refers to the type locality of the species, were collected in the middle reaches of the Jinsha River across the West of Sichuan and Yunnan Province, China.

**Diagnosis** *Gekko jinjiangensis* sp. nov. can be distinguished from its congeners by a combination of following characters: size small (SVL 50.2–61.6 mm, *n* = 13); nares in contact with rostral; interorbital scales between anterior corners of the eyes 20–24; ventral scales between mental and cloacal slit 146–169; midbody scale rows 111–149; ventral scale rows 31–47; subdigital lamellae on first toe 8–11, on fourth toe 11–15; no webbing in the fingers and toes; with tubercles on upper surface of fore and hind limbs; precloacal pores 4–5 in males and absent in the females; postcloacal unilateral tubercles 1–2; dorsal surface of body with 8–9 large greyish brown markings between nape and sacrum.

**Description of holotype** Adult male, SVL 54.7 mm; tail partially regenerated, TaL 46.3 mm (regeneration tail); head length longer than width (HL/HW=1.20), slightly depressed (HH/HL=0.46), distinct from neck; rostral irregular polygon, wider than highth (RW/RH=1.59) and relatively longer than mental (RW/MW=1.17), rostral groove present; rostral in contact with nostril, first supralabial and nasorostral; nostril suborbicular, touching rostral, first supralabial and three nasals (nasorostral, supranasal, postnasal); nasorostral enlarge in contact each other; supranasal equal to postnasal; internasal



**Figure 1** Phylogram based on the Bayesian analysis. Number above branches are Bayesian posteriorprobabilities (> 50%) and maximum likelihood bootstrap values, respectively.



**Figure 2** Holotype (CIB5334220115, male) of *Gekko jinjiangensis* sp. nov. A: Lateral view of head. B: dorsal view of snout. C: ventral view of chin. D: ventral view of left hand. E: ventral view of right hand. F: dorsal view of middle body. G: ventral view of precloacal region, showing five precloacal pores. H: lateral view of basal tail.

oval; snout moderate ( $SE/HL=0.39$ ), larger than eye diameter ( $SE/ED=1.43$ ); snout region medially concave from interorbital region to rostral; granular scales on anteriodorsal surface on head larger than those on posterior surface; preorbitals 12/11 (L/R); interorbitals 21; eye relatively large ( $ED/HL=0.27$ ); pupil vertical with crenulated margin; ear opening oval, obliquely oriented, smaller than eye ( $EAD/ED=0.35$ ); mental pentagons, equal in width and length ( $MW/ML=1.0$ ); two enlarged postmentals, hexagonal, longer than width; postmentals in

contact with mental and first infralabials anteriorly and six gular scales posteriorly; supralabial to midpoint of orbit 9/9 (supralabial to angle of jaw 11/11); infralabials to midpoint of orbit 7/6 (infralabials to angle of jaws 9/8).

Body slender, trunk relative long ( $AG/SVL=0.40$ ), dorsoventrally depressed in cross section; dorsal scales on body smooth, round or oval, granular, juxtaposed; dorsal tubercles 3–4 times the size of dorsal scales, smooth, round to oval, convex, surrounded by 8–10 dorsal scales; dorsal tubercles extending from occiput region to base of tail; tubercles in 16 regular rows at midbody; ventrolateral fold weakly developed, without tubercles; 43 ventral scales at midbody; ventral scales on abdomen much larger than dorsal or lateral scales, becoming smaller in chest and gular regions, flattened, subimbricated. Slightly enlarged precloacal scales bearing a continuous row of 5 precloacal pores; scales on dorsal surface of limbs larger than dorsum, smooth, round, or oval, granular, juxtaposed; scales on palms and soles smooth, round, or oval, granular, juxtaposed; scales on dorsal of digits, anterior surfaces of forearm, thigh, flattened, subimbricated.

Forelimbs and hindlimbs well developed, tubercles on fore and hind limbs are present, moderately long, slender; forearm and tibia moderately long; digits moderately expanded, both first finger and first toe, clawless, all remaining digits clawed; finger and toe webbing absent; subdigital lamellae, unnotched, undivided: 9–10–10–11–9 (left manus), 10–8–10–12–10 (right manus), 11–11–11–13–12 (left pes), 11–10–12–12–13 (right pes). Relative length of fingers: IV > III > V > II > I; relative length of toes: IV > III > V > II > I.

Tail regenerated; swollen at base; two postcloacal tubercle scales present on each lateral side; tail suddenly tapering from the basal swelling, slightly depressed, oval in section, covered above with small scales; tubercles on dorsal tail present only at base, similar with those on dorsal body, no large sharp tubercles present in rows on tail; dorsal scales of tail, smooth, oval, juxtaposed to weakly subimbricated in regular transverse

**Table 3** Mean (min–max) uncorrected pairwise distances (%) within and between species of the *Gekko japonicus* group based on ND2 sequences.

Species	1	2	3	4	5	6	7	8	9	10	11	12
1 <i>G. scabridus</i> MT449429												
2 <i>G. scabridus</i> MT449430	0.015											
3 <i>G. jinjiangensis</i> sp. nov. MT449431–36	0.109–0.111	0.118–0.122										
4 <i>G. jinjiangensis</i> sp. nov. MT449437–43	0.099–0.107	0.107–0.111	0–0.036									
5 <i>G. japonicus</i> JN019059	0.176	0.180	0.178–0.182	0.174–0.178								
6 <i>G. japonicus</i> JQ173423	0.176	0.180	0.174–0.178	0.171–0.174	0.004							
7 <i>G. japonicus</i> MN811642	0.176	0.180	0.174–0.178	0.171–0.174	0.004	0.000						
8 <i>G. hokouensis</i> JN019060	0.171	0.174	0.210–0.214	0.193–0.199	0.206	0.206	0.206					
9 <i>G. swinhonis</i> JN019061	0.169	0.176	0.189–0.191	0.182–0.189	0.191	0.191	0.191	0.193				
10 <i>G. auriverrucosus</i> JN019062	0.193	0.199	0.208–0.210	0.203–0.205	0.188	0.186	0.186	0.210	0.188			
11 <i>G. subpalmatus</i> JN019063	0.210	0.216	0.205–0.208	0.206–0.210	0.221	0.225	0.225	0.227	0.206	0.188		
12 <i>G. chinensis</i> JQ173409	0.214	0.221	0.225–0.229	0.214–0.218	0.225	0.225	0.225	0.223	0.221	0.270	0.246	
13 <i>Lepidodactylus moestus</i> JN019079	0.240	0.250	0.251–0.253	0.242–0.246	0.266	0.266	0.266	0.283	0.270	0.265	0.280	0.298

rows; ventral scales much larger than dorsal, smooth, and imbricated, with enlarged subcaudal plates.

**Color of the holotype in life (Figure 2)** In life, dorsal surfaces of head, neck and body light grey, scattered with 8 large light and dark brown wide irregular W-shaped patches from neck to the swollen section of tail; dorsal surfaces of limbs, flesh red. Dorsal part of limbs mottled with small, light blotches irregularly scattered; dorsal tail greyish, with single dark bands, regenerated portion yellow-brown without band; ventral skin creamy-yellow, ventral tail and regenerated tail creamy-white. Iris sliver with minute, dark brown reticulations, pupil solid black with a sliver edge.

**Color of holotype in preservative** In preservative (fixed in formalin, stored in 75% ethanol for 4 months), dorsal and lateral surfaces of head, body and limbs creamy-white with distinct dark grey flecks; tail similar to dorsal ground color with light grey bands and scattered small dark flecks; ventral body white, limbs, precloacal regions and tail creamy with minute dark grey pigment speckles on gular and limbs regions (Figure 3).

**Variation** The differences between the measurement data and the scales of the 13 specimens are shown in the Table 4. Male paratypes (CIB5133380021, CIB5334220090, CIB5334220088) with 4 distinct precloacal pores, holotype (CIB5334220115) with 5; paratypes CIB5133380021, CIB5133380026, CIB5133380024, CIB5334220114, CIB5133380047, CIB5334220089, CIB5133380025, CIB5133380017, CIB5133380019, CIB5334220090 and CIB5334220088 with one postcloacal tubercle, while paratype CIB5334220100 with two postcloacal tubercles similar with the holotype. A small internasal present in paratypes CIB5133380021, CIB5133380026, CIB5334220089, CIB5133380025, CIB5133380017, CIB5334220088, CIB5334220115, but absent in paratypes CIB5133380024, CIB5334220114, CIB5133380047,

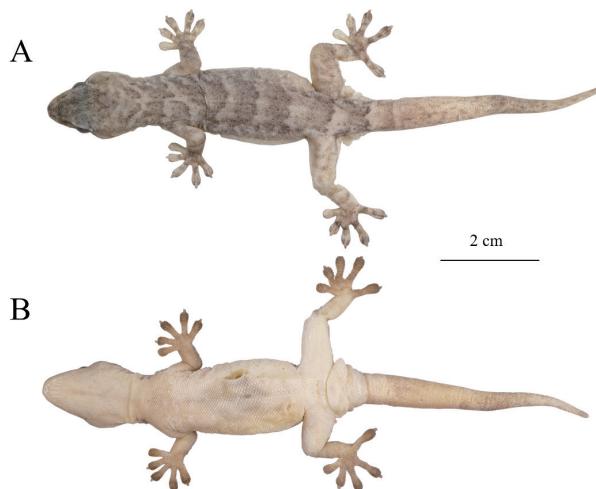


Figure 3 Holotype (CIB5334220115, male) of *Gekko jinjiangensis* sp. nov. in preservation. A: dorsal view. B: ventral view.

CIB5334220100, CIB5133380019, CIB5334220090. Dorsal coloration varies between specimens, paratypes CIB5133380019 and CIB5334220100 (Figure 4) dark brown, and the remaining are light colored. Dorsal surface of body with 8–9 large greyish brown markings between nape and sacrum. Among them the holotype and paratypes CIB5133380019, CIB5133380026, CIB5133380047, CIB5334220088, CIB5334220089, CIB5334220114 have 8 large greyish brown markings; the remaining type specimens are 9. Original tails with about 9–10 light brown and faint white transverse bands (CIB5133380024, CIB5133380047 have 10, CIB5133380021, CIB5133380026, CIB5334220090 have 9). The holotype and CIB5334220088, CIB5334220114, CIB5133380017, CIB5133380019, CIB5133380025 have an obscure dusky band from nostril through eye to ear-opening, the remaining type specimens have a clear and dark band. Regenerated tails (CIB5334220089, CIB5133380025, CIB5133380017, CIB5334220100, CIB5133380019, CIB5334220114, CIB5334220088 and CIB5334220115) shorter tail than original tails, and the scales on the ventral part of these tails are also more irregular.



Figure 4 Living female paratype of *Gekko jinjiangensis* sp. nov. Dorso-lateral view of CIB5334220100.

**Distribution and natural history** *Gekko jinjiangensis* sp. nov. is currently known from the middle reaches of the Jinsha River, Sichuan and Yunnan Province, China at elevations between 2000–2476 m a.s.l. The new species is nocturnal, inhabits shrubs or dry rocky cliffs in Jinsha River valley, and also found on walls of building (Figure 5). The breeding season is currently uncertain, no gravid female found during field work from late August 2019 and late July 2020.

**Comparison.** The undescribed species can clearly differ from the remaining species of the *G. japonicus* group by a unique suite of features. The new *Gekko* species differs from the members of the *G. japonicus* group as follows (Table 5).

The new species can be easily distinguished from *G. aaronbaueri* by having fewer supralabials and infralabials (7–10 versus 13 or 14 and 6–9 versus 10 or 11, respectively), fewer interorbital scales (20–24 versus 34–37), dorsal tubercle rows at midbody (12–16 versus absent), more scale rows around midbody (111–149 versus 98–104), fewer lamellae under first toe



**Figure 5** Habitat of *Gekko jinjiangensis* sp. nov. A: macrohabitat, dry-hot river valley in Benzilan Town, Deqin County, Yunnan Province. B, C, D: microhabitats. B: holotype CIB5334220115 found on small bushes in the Jinsha River valley. C: one individual hide in rock stretches on cliff after disturbance. D: one individual found on slope with bushes.

(8–11 versus 14–17), tubercles on limbs (present versus absent), tubercles on dorsal surface of tail (present versus absent), and a different dorsal flecks and bands pattern.

The new species differs from *G. adleri* by having fewer interorbital scales (20–24 versus 27–36), more dorsal tubercle rows at midbody (12–16 versus 7–11), no toes webbing (versus present), tubercles on fore limbs (present versus absent), fewer precloacal pores in males (4 or 5 versus 17–21), and a different head markings pattern.

The new species differs from *G. auriverrucosus* by having a nostril touching rostral (versus not touching in latter), by having fewer interorbital scales (20–24 versus 25), postmentals enlarged (versus not enlarged in latter), more lamellae under fourth toe (11–15 versus 6–8), fewer precloacal pores in males (4 or 5 versus 8–11).

The new species can be easily distinguished from *G. bonkowskii* by having fewer supralabials and infralabials (7–10 versus 12–14 and 6–9 versus 10 or 11, respectively), fewer interorbital scales (20–24 versus 26–27), dorsal tubercle rows at midbody (12–16 versus absent), no toes webbing (versus present), tubercles on limbs (present versus absent), fewer precloacal pores in males (4 or 5 versus 6), tubercles on dorsal surface of tail (present versus absent), and a different dorsal flecks and bands pattern.

The new species differs from *G. canhi* by having fewer supralabials and infralabials (7–10 versus 14 and 6–9 versus 10–12, respectively), fewer interorbital scales (20–24 versus 49 or 50), fewer scale rows at midbody (111–149 versus 205–227), fewer ventral scale rows at midbody (31–47 versus 49–51), fewer lamellae under first toe (8–11 versus 13–16), tubercles on fore limbs (present versus absent), tubercles on dorsal surface of tail

(present versus absent), and a different dorsal flecks pattern.

The new species differs from *G. chinensis* by having fewer interorbital scales (20–24 versus 35–48), dorsal tubercle rows at midbody (12–16 versus 10), no toes webbing (versus present), tubercles on fore limbs (present versus absent), fewer precloacal pores in males (4 or 5 versus 17–27); and a different dorsal flecks and bands pattern.

The new species differs from *G. hokouensis* by having fewer interorbital scales (20–24 versus 30–33), postmentals enlarged (versus not enlarged), tubercles on limbs (present versus absent); no back flecked or blotched (versus present), and a different dorsal flecks and bands pattern.

The new species differs from *G. kwangsiensis* by having fewer infralabials (6–9 versus 11–13), fewer interorbitals (20–24 versus 29–31); more dorsal tubercle rows at midbody (12–16 versus 9–11), fewer scales in a line from mental to the front of cloacal slit (146–169 versus 185–208), no toes webbing (versus present), tubercles on limbs (present versus absent), fewer precloacal pores in males (4 or 5 versus 9–11).

The new species differs from *G. liboensis* by having fewer supralabials and infralabials (7–10 versus 12 and 6–9 versus 11, respectively), fewer interorbital scales (20–24 versus 40), postmentals enlarged (versus not enlarged), dorsal tubercle rows at midbody (12–16 versus 10), more lamellae under fourth toe (11–15 versus 9), tubercles on limbs (present versus absent).

The new species can be easily distinguished from *G. melli* by having fewer interorbitals (20–24 versus 34–40); dorsal tubercle rows at midbody (12–16 versus absent), postmentals enlarged (versus not enlarged), fewer scales in a line from mental to the front of cloacal slit (146–169 versus 181–200), no toes webbing (versus present), tubercles on limbs (present versus absent), fewer precloacal pores in males (4 or 5 versus 9–11); tubercles on dorsal surface of tail (present versus absent), and a different head markings pattern.

The new species can be easily distinguished from *G. nadenensis* by having fewer supralabials and infralabials (7–10 versus 12–14 and 6–9 versus 10–12, respectively), fewer interorbitals (20–24 versus 28–30); fewer scales in a line from mental to the front of cloacal slit (146–169 versus 175–185), fewer lamellae under first toe (8–11 versus 13–15), no toes webbing (versus present), tubercles on limbs (present versus absent), fewer precloacal pores in males (4 or 5 versus 6); tubercles on dorsal surface of tail (present versus absent), and a different dorsal flecks and bands pattern.

The new species differs from *G. palmatus* by having fewer supralabials (7–10 versus 11–15), fewer interorbitals (20–24 versus 27–36); no toes webbing (versus present), tubercles on limbs (present versus absent), fewer precloacal pores in males (4 or 5 versus 23–30), and a different dorsal flecks pattern.

The new species can be easily distinguished from *G.*

**Table 4** The measurements (in mm) and morphological characters of the type series of *Gekko jinjiangensis* sp. nov. ("F/M" means the gender female and male respectively. "\*" means the length of regeneration tail; "/" means severed tail).

Measurements	CIB513 3380026	CIB513 3380024	CIB533 4220114	CIB513 3380047	CIB533 4220089	CIB513 3380025	CIB513 3380017	CIB533 4220100	CIB513 3380019	CIB533 4220115	CIB533 4220090	CIB533 4220088	CIB513 3380021	Mean ± SD	Range
F/M	F	F	F	F	F	F	F	F	F	M	M	M	M		
SVL	54.6	54.9	55.4	55.4	55.7	56.5	57.1	58	61.5	54.7	58.5	61.6	50.2	56.5 ± 3.0	50.2–61.6
TaL	58.8	62.7	46.3*	60.7	/	42.0*	/	/	/	46.3*	62.9	/	57	/	/
AG	24.3	23.6	25	25.9	20.2	24.2	25.4	24	26	22.1	24.6	24.7	23.9	24.2 ± 1.6	20.2–26.0
HL	13.2	13.4	13.8	12.8	14.3	12.2	12.9	15.1	14.6	14	14.5	15.5	12.1	13.7 ± 1.1	12.1–15.5
HW	11.2	10.5	10.2	11.4	11.3	9.2	11.2	11.8	12.3	11.7	11.9	12.3	10.1	11.2 ± 0.9	9.2–12.3
HH	6.1	6.4	5.7	6.6	5.9	4.9	6	6.1	6.8	6.4	6.7	7	6.6	6.2 ± 0.6	4.9–7.0
SE	5.2	6.1	5.2	5.3	6	5.3	5.9	6.1	6.2	5.5	6	7	5.4	5.8 ± 0.5	5.2–7.0
EE	4.7	5.4	4.8	5.6	5	3.8	5.2	5.1	5.7	6.1	5.4	5.5	4.6	5.1 ± 0.6	3.8–6.1
ED	3.6	3	3.9	3.2	3.4	3.3	3	3.5	3.3	3.8	3.5	3.7	3.3	3.4 ± 0.3	3.0–3.9
EAD	0.9	0.6	0.9	0.5	0.9	0.7	0.4	0.6	1	1.3	0.9	0.6	0.6	0.8 ± 0.2	0.4–1.3
RW	2.2	2.1	1.9	2.3	2.3	2	2.1	2.2	2.5	1.9	2.1	2.1	1.7	2.1 ± 0.2	1.7–2.5
RH	1	1	1.1	1.6	1.5	1.2	1.3	1.1	1.3	1.2	1.1	1.1	1.2	1.2 ± 0.2	1.0–1.6
ML	2	1.4	1.4	1.6	1.2	1.8	1.7	1.3	1.5	1.7	1.8	1.8	1.4	1.6 ± 0.2	1.2–2.0
MW	1.4	1.1	1.2	1.6	1.5	1.6	1.4	2.1	1.7	1.7	1.9	1.8	1.6	1.6 ± 0.3	1.1–2.1
CS	5/6	6/5	4/4	6/7	5/7	5/5	4/6	5/7	5/6	9/9	7/8	6/3	4/6		
N	3/3	3/3	3/3	3/3	3/3	3/3	3/3	3/3	3/3	3/3	3/3	3/3	3/3	3/3	3/3
I	1	0	0	0	1	1	1	0	0	1	0	1	1	1	1
SPL	8/8	9/9	9/10	8/8	9/10	9/9	9/9	9/9	9/9	8/8	8/8	9/8	7/8		
IFL	7/7	8/8	8/9	7/6	7/7	7/7	7/8	8/7	7/7	7/7	6/7	7/6	7/6		
IO	22	20	22	23	20	20	22	24	20	21	22	23	24		
PO	10/12	13/13	12/12	12/13	14/13	11/11	12/13	12/11	12/10	12/11	11/15	13/11	11/13		
PM	2	2	2	2	2	2	2	2	2	2	2	2	2		
GP	9	8	8	8	6	7	7	10	10	6	10	7	9		
DTR	12	13	14	15	14	13	12	15	14	16	13	15	13		
GSDT	8	10	9	9	9	10	9	10	10	8	9	9	9		
SMC	157	163	156	160	169	146	165	162	152	158	161	146	156		
SR	132	124	112	132	113	142	119	129	111	127	127	124	149		
V	37	37	44	47	39	38	31	39	34	43	47	37	35		
LF1	9/9	9/10	9/8	8/9	9/9	9/8	9/9	8/9	10/10	9/10	10/9	8/9	9/8		
LF4	11/11	13/12	13/14	12/11	12/12	11/12	12/12	11/13	13/13	11/12	13/13	11/11	11/10		
LT1	9/9	9/9	8/9	9/10	9/9	9/9	9/9	9/10	10/10	8/10	10/11	9/9	9/10		
LT4	13/11	14/14	13/14	12/13	14/14	12/13	13/15	14/13	13/12	13/12	14/14	12/13	13/13		
PP	0	0	0	0	0	0	0	0	0	5	4	4	4		
PAT	1/1	1/1	1/1	1/1	1/1	1/1	1/1	2/2	1/1	2/2	1/1	1/1	1/1		

Note: The morphological characters abbreviations are shown in Table 2.

*scientiadventura* by having fewer supralabials (7–10 versus 12–14), fewer interorbitals (20–24 versus 41–51), dorsal tubercle rows at midbody (12–16 versus absent), more scales in a line from mental to the front of cloacal slit (146–169 versus 118–140), fewer lamellae under first toe (8–11 versus 12–15); no toes webbing (versus present), tubercles on limbs (present versus absent), tubercles on dorsal surface of tail (present versus absent), and a different dorsal flecks and bands pattern.

The new species differs from *G. subpalmatus* by having fewer interorbitals (20–24 versus 32), postmentals enlarged (versus not enlarged), fewer dorsal tubercle rows at midbody (12–16 versus absent), fewer ventral scale rows at midbody (31–47 versus 48), more lamellae under fourth toe (11–15 versus 7–10), no toes webbing (versus present), tubercles on limbs (present versus absent), and a different dorsal

versus absent), tubercles on dorsal surface of tail (present versus absent), and a different dorsal flecks pattern.

The new species differs from *G. swinhonis* by having postmentals enlarged (versus not enlarged), more dorsal tubercle rows at midbody (12–16 versus 6–8), more lamellae under fourth toe (11–15 versus 6–9), fewer precloacal pores in males (4 or 5 versus 7–9); and a different dorsal flecks and bands pattern.

The new species can be easily distinguished from *G. sengchanthavongi* by having fewer interorbitals (20–24 versus 28–32), dorsal tubercle rows at midbody (12–16 versus absent), fewer scales in a line from mental to the front of cloacal slit (146–169 versus 175–184), no toes webbing (versus present), tubercles on limbs (present versus absent), tubercles on dorsal surface of tail (present versus absent), and a different dorsal

**Table 5** Morphological comparisons among the species of the *Gekko japonicus* group (modified after Luu *et al.*, 2017; Zhao *et al.*, 1999; Goris and Maeda, 2004; Zhou *et al.*, 1982). “-” means data unavailable; grey bold fonts represent the difference with the new species.

Characters	MaxSVL	SPL	IFL	N to R	I	IO	PM	DTR	SMC	SR	V	LT1	LT4	Web	Fore tubercles	Hind tubercles	Tail tubercles	PP	Marking	Flecked/ blotched	Banded
<i>G. jinjangensis</i> sp. nov.	616	7-10	6-9	1	0-1	20-24	1	12-16	146-169	111-149	31-47	8-11	11-15	0	1	1	4-5	0	0	1	
<i>G. aaronbaueri</i>	80	<b>13-14</b>	<b>10-11</b>	1	0-1	34-37	1	0-0	-	<b>98-104</b>	39-43	<b>14-17</b>	14-16	-	0	0	0	3-4	1	1	0
<i>G. adleri</i>	753	10-15	9-13	1	1-1	27-36	1	<b>7-11</b>	168-190	123-144	35-44	11-14	11-15	<b>1</b>	0	1	1	<b>17-21</b>	<b>1</b>	0	1
<i>G. auriverticatus</i>	69	9-11	9-11	0	0-1	25-25	0	16-20	-	-	-	6-8	<b>6-8</b>	0	1	1	1	<b>8-11</b>	0	0	1
<i>G. bonkowskii</i>	692	<b>12-14</b>	<b>10-11</b>	1	0-0	26-27	1	0-0	154-169	117-117	37-40	11-13	15-15	<b>1</b>	0	0	0	<b>6-6</b>	0	1	0
<i>G. canhi</i>	992	<b>14-14</b>	<b>10-12</b>	1	1-1	49-50	1	11-12	168-170	205-227	<b>49-51</b>	<b>13-16</b>	14-17	0	0	1	0	5-5	0	1	1
<i>G. chinensis</i>	72	10-14	9-13	1	1-1	35-48	1	<b>10-10</b>	156-167	118-140	37-39	8-10	9-12	<b>1</b>	0	1	1	<b>17-27</b>	0	1	0
<i>G. hokouensis</i>	70	10-14	8-11	1	1-1	30-33	0	12-18	153-174	119-130	36-43	8-11	15-18	0	0	0	1	5-9	0	1	0
<i>G. japonicus</i>	74	9-13	8-13	1	0-1	32-35	1	9-14	169-188	130-144	39-44	10-12	14-16	0	1	1	1	6-9/4-8	0	0	1
<i>G. kwangsiensis</i>	697	10-12	11-13	1	0-1	29-31	1	9-11	<b>185-208</b>	143-156	41-45	11-13	13-18	<b>1</b>	0	0	1	9-11	0	0	1
<i>G. liboenensis</i>	85	<b>12-12</b>	<b>11-11</b>	1	0-0	40-40	0	10-10	-	-	-	8-8	<b>9-9</b>	0	0	0	-	-	0	0	1
<i>G. melii</i>	846	10-13	9-12	1	1-1	34-40	0	0-0	181-200	147-160	43-49	10-12	11-14	<b>1</b>	0	0	0	9-11	<b>1</b>	0	1
<i>G. nadensis</i>	77.1	<b>12-14</b>	<b>10-12</b>	1	0-0	28-30	1	0-0	<b>175-185</b>	123-140	38-40	<b>13-15</b>	14-16	<b>1</b>	0	0	0	6-6	<b>1</b>	1	0
<i>G. palmatus</i>	79.7	<b>11-15</b>	9-13	1	0-3	27-36	1	4-12	160-191	116-147	36-47	10-13	10-16	<b>1</b>	0	0	1	<b>23-30</b>	0	1	1
<i>G. scientiaadvena</i>	73	<b>12-14</b>	9-13	1	0-0	41-51	1	0-0	<b>118-140</b>	139-143	38-48	<b>12-15</b>	14-17	<b>1</b>	0	0	0	5-8	<b>1</b>	<b>1</b>	0
<i>G. scabridus</i>	64	9-11	9-11	1	1-2	30-30	1	<b>17-21</b>	-	-	-	6-9	<b>7-9</b>	0	1	1	1	<b>10-15</b>	0	1	1
<i>G. subpalmatus</i>	72	8-12	7-12	1	1-1	32-32	0	0-0	-	-	<b>48-48</b>	7-9	<b>7-10</b>	1	0	0	0	5-11	0	1	1
<i>G. swinhonis</i>	66	7-12	7-11	1	-	23-24	0	<b>6-8</b>	-	-	40-40	6-9	<b>6-9</b>	0	1	1	-	<b>7-9</b>	0	1	0
<i>G. sengchanthaongi</i>	77.3	8-10	6-7	1	0-0	28-32	1	0-0	<b>175-184</b>	120-135	35-43	11-14	13-17	<b>1</b>	0	0	0	4-5	0	1	1
<i>G. shibatai</i>	70.9	10-13	<b>10-14</b>	1	0-1	37-52	0	5-14	-	114-134	-	-	9-16	0	0	0	1	<b>0-3</b>	0	1	0
<i>G. similignum</i>	58.9	<b>12-14</b>	<b>11-11</b>	1	1-1	<b>46-48</b>	0	<b>11-11</b>	-	144-153	-	11-13	12-14	<b>1</b>	0	0	1	<b>17-17</b>	0	1	0
<i>G. taibaensis</i>	69	9-10	8-10	1	-	28-28	-	-	-	-	6-7	<b>7-8</b>	-	-	-	-	4-6	0	1	1	
<i>G. tawaensis</i>	71	<b>15-15</b>	13-13	1	2-2	-	0	0-0	-	-	10-10	12-12	0	0	0	0	0-0	0	1	1	
<i>G. thakhienensis</i>	79.2	<b>12-14</b>	<b>10-11</b>	1	0-0	22-26	1	0-0	165-174	110-116	32-40	11-13	14-15	<b>1</b>	0	0	0	1-5	0	1	0
<i>G. truongi</i>	95.9	<b>13-15</b>	<b>11-13</b>	1	0-1	<b>45-48</b>	1	<b>0-0</b>	160-172	131-143	35-36	11-13	15-17	0	0	0	0	<b>10-11</b>	0	1	1
<i>G. vertebralis</i>	69.2	10-15	<b>10-15</b>	1	0-2	35-50	0	2-12	-	112-139	-	-	9-17	0	0	0	0-1	0	1	0	
<i>G. wenxianensis</i>	59	<b>12-12</b>	<b>11-11</b>	1	1-1	-	-	<b>10-10</b>	-	-	42-44	<b>6-6</b>	<b>9-9</b>	0	0	1	-	<b>6-8</b>	0	1	0
<i>G. yakunensis</i>	72	12-13	9-13	1	1-1	-	0	-	-	-	10-10	15-15	0	0	0	1	<b>6-8</b>	0	1	0	

Notes: Character abbreviations (from left to right): MaxSVL: Maximum SVL (mm); SPL: SPL (min)-(max); IFL: IFL (min)-(max); N to R: Nostril touching rostral; I: I (min)-(max); IO: IO (min)-(max); LT1: LT1 (min)-(max); LT4: LT4 (min)-(max); LT: LT (min)-(max); SR: SR (min)-(max); SMC: SMC (min)-(max); V: V (min)-(max); DTR: DTR (min)-(max); Web: Toes webbed (present=1, absent=0); Fore tubercles: Tubercles on fore limbs (present=1, absent=0); Hind tubercles: Tubercles on hind limbs (present=1, absent=0); Tail tubercles: Tubercles on dorsal surface of tail (present=1, absent=0); PP: PP (in males, min-(in males, max); Marking: Marking on upper side of head; Flecked/blotched: Back flecked or blotched; Back banded: Back banded. In the last three characters: number "1" represents similar patterns, "0" represents different patterns.

flecks pattern.

The new species differs from *G. shibatai* by having fewer infralabials (6–9 versus 10–14), fewer interorbitals (20–24 versus 37–52), postmentals enlarged (versus not enlarged), tubercles on limbs (present versus absent), more precloacal pores in males (4 or 5 versus 0–3), and a different dorsal flecks and bands pattern.

The new species can be easily distinguished from *G. similignum* by having fewer supralabials and infralabials (7–10 versus 12–14 and 6–9 versus 11, respectively), fewer interorbitals (20–24 versus 46–48), postmentals enlarged (versus not enlarged), more dorsal tubercle rows at midbody (12–16 versus 11), no toes webbing (versus present), tubercles on limbs (present versus absent), fewer precloacal pores in males (4 or 5 versus 17), and a different dorsal flecks and bands pattern.

The new species differs from *G. taibaiensis* by having fewer interorbitals (20–24 versus 28), more lamellae under first toe (11–15 versus 6 or 7), and more lamellae under fourth toe (11–15 versus 7 or 8), and a different dorsal flecks pattern.

The new species differs from *G. tawaensis* by having fewer supralabials and infralabials (7–10 versus 15 and 6–9 versus 13, respectively), postmentals enlarged (versus not enlarged), fewer intersupranasals (0–1 versus 2–2), dorsal tubercle rows at midbody (12–16 versus absent), tubercles on limbs (present versus absent), tubercles on dorsal surface of tail (present versus absent), and a different dorsal flecks pattern.

The new species differs from *G. thakhekensis* by having fewer supralabials and infralabials (7–10 versus 12–14 and 6–9 versus 10–11, respectively), dorsal tubercle rows at midbody (12–16 versus absent), no toes webbing (versus present), tubercles on limbs (present versus absent), tubercles on dorsal surface of tail (present versus absent), and a different dorsal flecks and bands pattern.

The new species can be easily distinguished from *G. truongi* by having fewer supralabials and infralabials (7–10 versus 13–15 and 6–9 versus 11–13, respectively), fewer interorbitals (20–24 versus 45–48), dorsal tubercle rows at midbody (12–16 versus absent), tubercles on limbs (present versus absent), fewer precloacal pores in males (4 or 5 versus 10 or 11); tubercles on dorsal surface of tail (present versus absent), and a different dorsal flecks pattern.

The new species differs from *G. vertebralis* by having fewer infralabials (6–9 versus 10–15), fewer interorbitals (20–24 versus 35–50), postmentals enlarged (versus not enlarged), tubercles on limbs (present versus absent), more precloacal pores in males (4 or 5 versus 0 or 1); tubercles on dorsal surface of tail (present versus absent), and a different dorsal flecks and bands pattern.

The new species differs from *G. wenxianensis* by having fewer supralabials and infralabials (7–10 versus 12 and 6–9 versus 11, respectively), more dorsal tubercle rows at midbody (12–16 versus 10), more lamellae under first toe (11–15 versus 6), more

lamellae under fourth toe (11–15 versus 9), tubercles on fore limbs (present versus absent), fewer precloacal pores in males (4 or 5 versus 6–8), and a different dorsal flecks and bands pattern.

The new species differs from *G. yakuensis* by having fewer supralabials (7–10 versus 12–13), postmentals enlarged (versus not enlarged), tubercles on limbs (present versus absent), fewer precloacal pores in males (4 or 5 versus 6–8), and a different dorsal flecks and bands pattern.

*G. japonicus* is the species with the highest morphological similarity to the new species, but the phylogenetic relationships and genetic distance make it easy to distinguish between the two species (uncorrected *p*-distance 17.1%–18.2%). Morphologically, the new species differs from *G. japonicus* by having fewer interorbital scales (20–24 versus 32–35); no toes webbing (versus relative obvious); the tubercle scales on thigh distinct (versus generally without) (Tian et al., 1986; Stejneger, 1901).

*G. scabridus* is the species with the closest phylogenetic relationship and genetic distance to the new species. The two species are easily distinguished by their morphological features (Figure 6). The new species differs from *G. scabridus* by having fewer interorbitals (20–24 versus 30), fewer dorsal tubercles

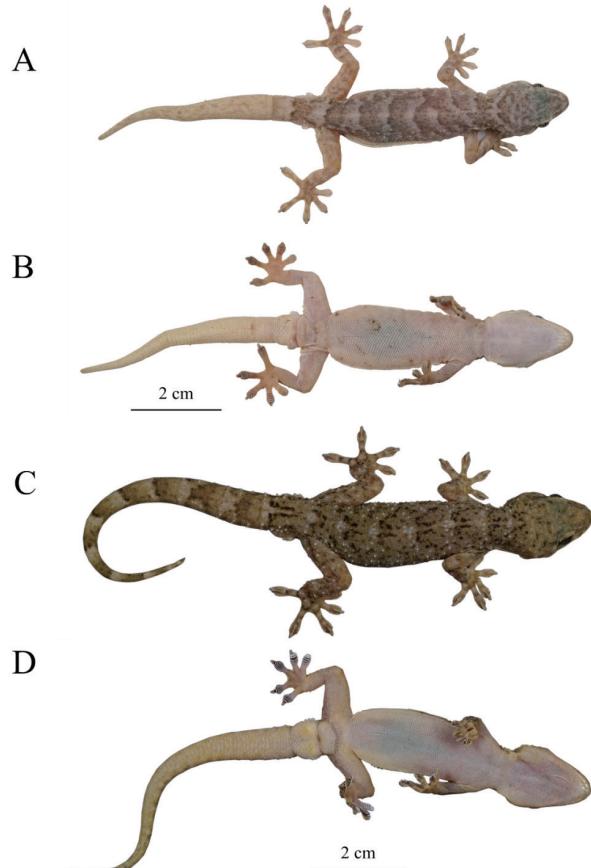
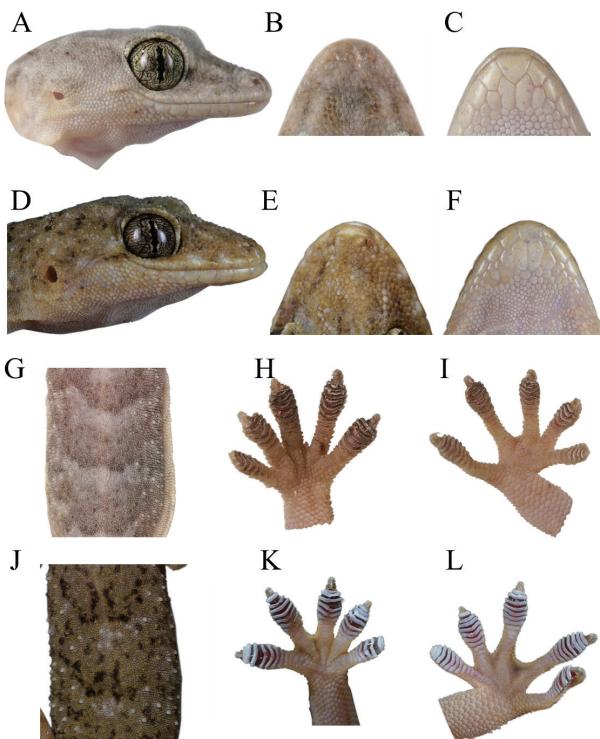


Figure 6 Holotype (CIB5334220115, male) of *Gekko jinjiangensis* sp. nov. in life and *G. scabridus* (CIBYN201909200, male) from Yanbian, Sichuan Province: A, C: dorsal view. B, D: ventral view.

rows at midbody (12–16 versus 17–21), more lamellae under fourth toe (11–15 versus 7–9) (Figure 7), fewer precloacal pores in males (4 or 5 versus 10–15) (Figure 8), no toes webbing (versus relative obvious), large markings on the back (versus dark brown and mesh spots).

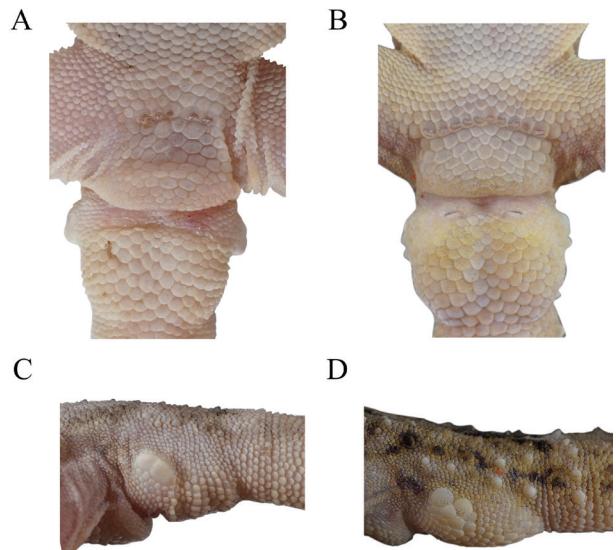


**Figure 7** Sculation on head, trunk, and digits of *Gekko jinjiangensis* sp. nov. (holotype CIB5334220115) and *G. scabridus* (CIBYN201909200). A: lateral view of head. B: dorsal view of snout. C: ventral view of chin of *Gekko jinjiangensis* sp. nov. D: lateral view of head. E: dorsal view of snout. F: ventral view of chin of *G. scabridus*. G: dorsal view of trunk. H: ventral view of left hand. I: ventral view of right foot of *Gekko jinjiangensis* sp. nov. J: dorsal view of trunk. K: ventral view of right hand. L: ventral view of left feet of *G. scabridus*.

#### 4. Discussion

Yang and Rao (2008) recorded *G. japonicus* from Benzilan of Deqin, Yunnan Prov., which is the type location of the new species. This record should be referred to the new species as it matches the diagnosis of the new species morphologically. Besides, Yang and Rao (2008) noted that this species is common, and *G. jinjiangensis* sp. nov. is common at its distribution area during our field work last near two months (August 2019 and July 2020). Detailed distribution range, population size and states, and threats of the species is still not known enough, further surveys are recommended to better understand the distribution and population status of the species.

The new species is the highest distributed species of *Gekko* from the Qinghai-Tibet Plateau with a highest elevation range



**Figure 8** Male sexual character and basal tail of *Gekko jinjiangensis* sp. nov. (holotype CIB5334220115, male) and *G. scabridus* (CIBYN201909200, male). A: precloacal region of *Gekko jinjiangensis* sp. nov. B: precloacal region of *G. scabridus*. C: lateral view of basal tail of *Gekko jinjiangensis* sp. nov. D: lateral view of basal tail of *G. scabridus*.

(2000 and 2476 m a.s.l.), the major habitat of *Gekko jinjiangensis* sp. nov. is the dry-hot river valley in the middle of Jinsha River. We speculate that the reason for the radiation to the Tibetan Plateau is that the meridional dry hot river valley provides better hydrothermal conditions. The breeding period is presumed to be before July (May–June), as there are no females carrying eggs at July and August, but at the same time, more young individuals were found in the wild. During the field investigation, far more females were encountered than males. Two possible explanations to this phenomenon are possible high parthenogenesis rate and female biased sex determination during embryogenesis due to higher environmental temperature (Pieau, 1996).

At present, China (20 species) has the highest diversity of *Gekko* in East and Southeast Asia, followed by the Philippines (17 species), Thailand (16 species) and Vietnam (14 species) (Uetz, 2020). Among them, 12 species are endemic to China. The *Gekko* species of China belong to 4 gecko subgenera: *Japonigekko*, *Gekko*, *Ptychozoon*, *Archipelagekko* (Wood *et al.*, 2020), mostly distributed in tropical and subtropical regions south of the Qinling Mountains, fewer in north regions of the temperate zone. The descriptions of the new species indicated that widespread species such as the *G. japonicus* and *G. swinhonis* may include cryptic species and need to be checked seriously. So, we suggest that a broader sampling strategy and molecular re-identification is necessary to clarify the taxonomy and phylogeny of Chinese geckos.

**Acknowledgements** This study was supported by the

Second Tibetan Plateau Scientific Expedition and Research Program (STEP, 2019QZKK05010503), the Biodiversity Survey and Assessment Project of the Ministry of Ecology and Environment, China (2019HJ2096001006) to Feng XIE and Yin QI. We thank Jianyi FENG, Lei FU for their help in the field. We are also grateful to Mr. Xianguang GUO and Ke JIANG for their very helpful advices, and the local forestry administration for their support and help in our field work and issuing relevant permits.

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Handling Editor: Chen YANG

**How to cite this article:**

Hou Y. M., Shi S. C., Wang G., Shu G. C., Zheng P. Y., Qi Y., Liu G. H., Jiang J. P., Xie F. A New Species of the *Gekko japonicus* Group (Squamata: Gekkonidae) from Southwest China. *Asian Herpetol Res*, 2021, 12(1): 36–48.  
DOI: 10.16373/j.cnki.ahr.200064